

p#19



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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/349,915B

DATE: 07/24/2002
 TIME: 16:32:54

Input Set : A:\SEQLIST.txt
 Output Set: N:\CRF3\07242002\I349915B.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
 C--> 6 (i) APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
 7 Gray, Gary S., Rennert, Paul D.
 9 (ii) TITLE OF INVENTION: Methods For Selectively Stimulating
 10 Proliferation Of T-Cells
 12 (iii) NUMBER OF SEQUENCES: 14
 14 (iv) CORRESPONDENCE ADDRESS:
 15 (A) ADDRESSEE: HALE AND DORR LLP
 16 (B) STREET: 60 State Street
 17 (C) CITY: Boston
 18 (D) STATE: Massachusetts
 19 (E) COUNTRY: USA
 20 (F) ZIP: 02109
 22 (v) COMPUTER READABLE FORM:
 23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: IBM PC compatible
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 28 (vi) CURRENT APPLICATION DATA:
 C--> 29 (A) APPLICATION NUMBER: US/09/349,915B
 C--> 30 (B) FILING DATE: 01-Aug-2000
 31 (C) CLASSIFICATION:
 33 (vii) PRIOR APPLICATION DATA:
 34 (A) APPLICATION NUMBER: US 08/403,253
 35 (B) FILING DATE: March 10, 1995
 36 (A) APPLICATION NUMBER: US 08/253,964
 37 (B) FILING DATE: 3 JUNE 1994
 38 (A) APPLICATION NUMBER: US 08/073,223
 39 (B) FILING DATE: 4 JUNE 1993
 40 (A) APPLICATION NUMBER: US 08/200,947
 41 (B) FILING DATE: 23 FEB 1994
 42 (A) APPLICATION NUMBER: US 07/864,805
 43 (B) FILING DATE: 7 APR 1992
 44 (A) APPLICATION NUMBER: US 08/247,505
 45 (B) FILING DATE: 23 MAY 1994
 46 (A) APPLICATION NUMBER: US 07/864,866
 47 (B) FILING DATE: 7 APR 1992
 48 (A) APPLICATION NUMBER: US 08/218,155
 49 (B) FILING DATE: 25 MAR 1994
 50 (A) APPLICATION NUMBER: US 07/864,807
 51 (B) FILING DATE: 7 APR 1992
 52 (A) APPLICATION NUMBER: US 07/902,467

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53 (B) FILING DATE: 16 JUNE 1992
54 (A) APPLICATION NUMBER: US 07/275,433
55 (B) FILING DATE: 23 NOV 1988
57 (viii) ATTORNEY/AGENT INFORMATION:
58 (A) NAME: Superko, Colleen
59 (B) REGISTRATION NUMBER: 39,850
60 (C) REFERENCE/DOCKET NUMBER: 36119-125(US10)
62 (ix) TELECOMMUNICATION INFORMATION:
63 (A) TELEPHONE: (617) 526-6564
64 (B) TELEFAX: (617) 526-5000
67 (2) INFORMATION FOR SEQ ID NO: 1:
69 (i) SEQUENCE CHARACTERISTICS:
71 (A) LENGTH: 1491 base pairs
72 (B) TYPE: nucleic acid
73 (C) STRANDEDNESS: double
74 (D) TOPOLOGY: linear
76 (ii) MOLECULE TYPE: cDNA to mRNA
78 (iii) HYPOTHETICAL: no
80 (iv) ANTI-SENSE: no
82 (vi) ORIGINAL SOURCE:
84 (A) ORGANISM: Homo sapien
85 (F) TISSUE TYPE: lymphoid
86 (G) CELL TYPE: B cell
87 (H) CELL LINE: Raji
89 (vii) IMMEDIATE SOURCE:
91 (A) LIBRARY: cDNA in pCDM8 vector
92 (B) CLONE: B7, Raji clone #13
94 (viii) POSITION IN GENOME:
96 (A) CHROMOSOME/SEGMENT: 3
98 (ix) FEATURE:
100 (A) NAME/KEY: Open reading frame (translated region)
101 (B) LOCATION: 318 to 1181 bp
102 (C) IDENTIFICATION METHOD: similarity to other pattern
104 (ix) FEATURE:
106 (A) NAME/KEY: Alternate polyadenylation signal
107 (B) LOCATION: 1474 to 1479 bp
108 (C) IDENTIFICATION METHOD: similarity to other pattern
110 (x) PUBLICATION INFORMATION:
112 (A) AUTHORS: FREEMAN, GORDON J.
113 FREEDMAN, ARNOLD S.
114 SEGIL, JEFFREY M.
115 LEE, GRACE
116 WHITMAN, JAMES F.
117 NADLER, LEE M.
119 (B) TITLE: B7, A New Member Of The Ig Superfamily With
120 Unique Expression On Activated And Neoplastic B Cells
121 (C) JOURNAL: The Journal of Immunology
122 (D) VOLUME: 143
123 (E) ISSUE: 8

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124          (F) PAGES: 2714-2722
125          (G) DATE: 15-OCT-1989
C--> 126      (K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 1491
128          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
130 CCAAAGAAAA AGTGATTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT   60
132 GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTCTC TCAGCAAGCT  120
134 GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT  180
136 GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT  240
138 TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTTGGCTTT CACTTTTGAC  300
140 CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC  353
141          Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser
142          -30                                -25
145 AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT   401
146 Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu
147          -20                                -15                                -10
150 TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA   449
151 Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu
152          -5                                1                                5                                10
155 GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG GCA   497
156 Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala
157          15                                20                                25
160 CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT ATG   545
161 Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met
162          30                                35                                40
165 ATG TCT GGG GAC ATG AAT ATA TGG CCC GAG TAC AAG AAC CGG ACC ATC   593
166 Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile
167          45                                50                                55
170 TTT GAT ATC ACT AAT AAC CTC TCC ATT GTG ATC CTG GCT CTG CGC CCA   641
171 Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro
172          60                                65                                70
175 TCT GAC GAG GGC ACA TAC GAG TGT GTT GTT CTG AAG TAT GAA AAA GAC   689
176 Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp
177          75                                80                                85                                90
180 GCT TTC AAG CGG GAA CAC CTG GCT GAA GTG ACG TTA TCA GTC AAA GCT   737
181 Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala
182          95                                100                                105
185 GAC TTC CCT ACA CCT AGT ATA TCT GAC TTT GAA ATT CCA ACT TCT AAT   785
186 Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn
187          110                                115                                120
190 ATT AGA AGG ATA ATT TGC TCA ACC TCT GGA GGT TTT CCA GAG CCT CAC   833
191 Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His
192          125                                130                                135
195 CTC TCC TGG TTG GAA AAT GGA GAA GAA TTA AAT GCC ATC AAC ACA ACA   881
196 Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr
197          140                                145                                150
200 GTT TCC CAA GAT CCT GAA ACT GAG CTC TAT GCT GTT AGC AGC AAA CTG   929
201 Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu
202          155                                160                                165                                170
205 GAT TTC AAT ATG ACA ACC AAC CAC AGC TTC ATG TGT CTC ATC AAG TAT   977

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206 Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr
207           175           180           185
210 GGA CAT TTA AGA GTG AAT CAG ACC TTC AAC TGG AAT ACA ACC AAG CAA 1025
211 Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln
212           190           195           200
215 GAG CAT TTT CCT GAT AAC CTG CTC CCA TCC TGG GCC ATT ACC TTA ATC 1073
216 Glu His Phe Pro Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile
217           205           210           215
220 TCA GTA AAT GGA ATT TTT GTG ATA TGC TGC CTG ACC TAC TGC TTT GCC 1121
221 Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala
222           220           225           230
224 CCA AGA TGC AGA GAG AGA AGG AGG AAT GAG AGA TTG AGA AGG GAA AGT 1169
225 Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser
226 235           240           245           250
229 GTA CGC CCT GTA TAACAGTGTC CGCAGAAGCA AGGGGCTGAA AAGATCTGAA 1221
230 Val Arg Pro Val
233 GGTAGCCTCC GTCATCTCTT CTGGGATACA TGGATCGTGG GGATCATGAG GCATTCTTCC 1281
236 CTTAACAAAT TTAAGCTGTT TTACCCACTA CCTCACCTTC TTAAAAACCT CTTTCAGATT 1341
239 AAGCTGAACA GTTACAAGAT GGCTGGCATC CCTCTCCTTT CTCCCCATAT GCAATTTGCT 1401
242 TAATGTAACC TCTTCTTTTG CCATGTTTCC ATTCTGCCAT CTTGAATTGT CTTGTCAGCC 1461
245 AATTCATTAT CTATTAAACA CTAATTTGAG 1491

```

C--> 248 (2) INFORMATION FOR SEQ ID NO: 2:

250 (i) SEQUENCE CHARACTERISTICS:

252 (A) LENGTH: 288 amino acids

253 (B) TYPE: amino acid

C--> 254 (D) TOPOLOGY: linear

256 (ii) MOLECULE TYPE: protein

258 (A) DESCRIPTION: B cell activation antigen; natural ligand

W--> 259 for CD28 T cell surface antigen; transmembrane protein

261 (ix) FEATURE:

263 (A) NAME/KEY: signal sequence

264 (B) LOCATION: -34 to -1

265 (C) IDENTIFICATION METHOD: amino terminal sequencing of

266 soluble protein

267 (D) OTHER INFORMATION: hydrophobic

269 (ix) FEATURE:

271 (A) NAME/KEY: extracellular domain

272 (B) LOCATION: 1 to 208

273 (C) IDENTIFICATION METHOD: similarity with known

274 sequence

277 (ix) FEATURE:

279 (A) NAME/KEY: transmembrane domain

280 (B) LOCATION: 209 to 235

281 (C) IDENTIFICATION METHOD: similarity with known

282 sequence

285 (ix) FEATURE:

287 (A) NAME/KEY: intracellular domain

288 (B) LOCATION: 236 to 254

289 (C) IDENTIFICATION METHOD: similarity with known

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Input Set : A:\SEQLST.txt

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290 sequence
293 (ix) FEATURE:
295 (A) NAME/KEY: N-linked glycosylation
296 (B) LOCATION: 19 to 21
297 (C) IDENTIFICATION METHOD: similarity with known
298 sequence
301 (ix) FEATURE:
303 (A) NAME/KEY: N-linked glycosylation
304 (B) LOCATION: 55 to 57
305 (C) IDENTIFICATION METHOD: similarity with known
306 sequence
309 (ix) FEATURE:
311 (A) NAME/KEY: N-linked glycosylation
312 (B) LOCATION: 64 to 66
313 (C) IDENTIFICATION METHOD: similarity with known
314 sequence
317 (ix) FEATURE:
319 (A) NAME/KEY: N-linked glycosylation
320 (B) LOCATION: 152 to 154
321 (C) IDENTIFICATION METHOD: similarity with known
322 sequence
325 (ix) FEATURE:
327 (A) NAME/KEY: N-linked glycosylation
328 (B) LOCATION: 173 to 175
329 (C) IDENTIFICATION METHOD: similarity with known
330 sequence
333 (ix) FEATURE:
335 (A) NAME/KEY: N-linked glycosylation
336 (B) LOCATION: 177 to 179
337 (C) IDENTIFICATION METHOD: similarity with known
338 sequence
341 (ix) FEATURE:
343 (A) NAME/KEY: N-linked glycosylation
344 (B) LOCATION: 192 to 194
345 (C) IDENTIFICATION METHOD: similarity with known
346 sequence
349 (ix) FEATURE:
351 (A) NAME/KEY: N-linked glycosylation
352 (B) LOCATION: 198 to 200
353 (C) IDENTIFICATION METHOD: similarity with known
354 sequence
357 (ix) FEATURE:
359 (A) NAME/KEY: Ig V-set domain
360 (B) LOCATION: 1 to 104
361 (C) IDENTIFICATION METHOD: similarity with known
362 sequence
365 (ix) FEATURE:
367 (A) NAME/KEY: Ig C-set domain
368 (B) LOCATION: 105 to 202

VERIFICATION SUMMARY

DATE: 07/24/2002

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Input Set : A:\SEQLST.txt

Output Set: N:\CRF3\07242002\I349915B.raw

L:6 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:126 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:248 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:254 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:388 M:220 C: Keyword misspelled or invalid format, [(K) RELEVANT RESIDUES IN SEQ ID NO:]
L:675 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:850 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12